Assessment of chloroquine resistance of Plasmodium in patients attending malaria clinic in a government general hospital, Kurnool; Strategies to prevent chloroquine resistance

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Background: Prevalence of chloroquine resistant malaria is on a rise and our area is one of the declared endemic zones for malaria. Recent mortality trends of the disease have increased considerably seeking immediate modification in the treatment guidelines to decrease the complications and thus the mortality of the disease. We have attributed the present condition to the chloroquine resistance, the drug which is used to treat the disease in this area for so long. Even the effective surveillance system fails in decreasing the mortality figures by following the prescribed treatment guidelines. Hence, we have undertaken this project to assess the drug resistance and to state new treatment guidelines in the areas where chloroquine resistant malaria is rampant.

Methods: 250 patients are taken as sample in this project. After diagnosing them as Malaria by peripheral smear and IgM antibody detection tests, the patients are prescribed chloroquine tablets as per the treatment guidelines in this region for 3 days closely watching them for complications. The number of patients cured of the disease are noted and the number of uncured cases are assessed for the continuation of symptoms. The percentage of cured to uncured is calculated and this serves as an evaluation tool for chloroquine resistance. The Uncured subjects are prescribes Tablet Artesunate for 3 days.

Results: 106 patients are not cured after Standard chloroquine treatment and prescribed Artesunate treatment.

144 patients are cured after the chloroquine treatment.

% of cured patients = 57.6%

% of uncured patients = 42.4%

The ratio of Uncured to Cured = 0.736

the ratio >0.5

Full details will be submitted in the conference.

Conclusion: As the Ratio of Cured to Uncured is greater than 0.5 in this area, We want to intervene in the modifications of the standard treatment guidelines by introducing Artesunate instead of Chloroquine for the Patients suffering from Malaria in Our region. Any Endemic region with the ratio of Uncured to cured >O.5 should modify the treatment guidelines to decrease the complication rates and thus the mortality caused by this disease. For the regions with the ratio less than 0.5, Co-prescription of Artesunate is advised instead of relying only on Chloroquine.

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Blood microfilarial stage specific gene expression profile of *Brugia malayi*

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Background: Lymphatic filariasis, a mosquito-borne disease, is mainly caused by the nematodes *Wuchereria bancrofti* and *Brugia malayi*. The adult worms reside in the lymphatic vessels where they cause damage and the female release an abundance of offsprings (microfilariae; Mf) into the host's circulatory system. The Mf stage is associated with disease transmission, complex disease pathology, and host immunomodulation. Potential targets from the Mf stage for drug and vaccine development were investigated in order to reduce Mf density, improve disease morbidity, and prevent disease transmission.

Methods: The Filarial Nematode Oligonucleotide Array-Version 2 (BmV2array) slides comprising 18,153 oligonucleotide elements in duplicate that represent expressed genes and predicted ORFs from *B. malayi*, *Onchocerca volvulus*, *Wuchereria bancrofti*, and *Wolbachia*, were used to investigate gene expression changes in triplicate. 300,000 *B. malayi* Mf cultured *in vitro* to identify potential therapeutic targets.

Results: By 48 hours, significant increase of Mf gene expression was found in succinate dehydrogenase, malate dehydrogenase, NADH dehydrogenase, and cytochrome, which are important in glycolysis/gluconeogenesis, citrate cycle, ubiquinone biosynthesis, and oxidative phosphorylation, respectively. Furthermore, expression of immunomodulatory genes (e.g., macrophage inhibitory factor, transforming growth factor beta, serpin, and glutathione peroxidase), cathepsin-like cysteine protease, microfilarial sheath protein, motility genes (e.g., actin, myosin, tropomyosin, tubulin, and calmodulin), and ribosomal RNA were also found upregulated.

Conclusion: Microarray analysis is a valuable screening tool for identifying stage specific *B. malayi* Mf genes and related metabolic pathways. The roles of these genes as a target for developing novel antifilarial drugs or vaccines should be verified.

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Nitric oxide synthase immunity in the malaria non-vector *Anopheles culicifacies* species B: a putative transmission blocking *Plasmodium vivax* immune responsive mechanism for refractoriness

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Background: Innate immune-related anti-parasite defenses mounted by *Anopheles* may suppress the growth of *Plasmodium* in mosquitoes. Nitric oxide (NO) produced by the action of an inducible NO synthase (NOS) and its